

SEQUENCE LISTING

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<120> SUPERFICIAL ZONE PROTEIN AND METHODS OF
MAKING AND USING SAME

<130> 07083.0008US

<150> 60/258,920
<151> 2000-12-29

<160> 11

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 1
Asp Glu Ala Gly Ser Gly
1 5

<210> 2
<211> 188
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 2
Met Ala Trp Lys Thr Leu Pro Ile Tyr Leu Leu Leu Leu Ser Val
1 5 10 15
Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly
20 25 30
Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr
35 40 45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
 50 55 60
 Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg
 65 70 75 80
 Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
 85 90 95
 Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val Lys Asp Asn Lys Lys
 100 105 110
 Asn Arg Thr Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu
 115 120 125
 Ala Gly Ser Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp
 130 135 140
 Thr Ser Thr Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr
 145 150 155 160
 Thr Ala Lys Pro Ile Asn Pro Arg Pro Gln Ser Ser Pro Asn Ser Asp
 165 170 175
 Thr Ser Lys Glu Thr Ser Leu Thr Val Asn Lys Glu
 180 185

<210> 3
 <211> 538
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 3
 Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro Glu Leu Ser
 1 5 10 15
 Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro Lys Glu Pro Gly
 20 25 30
 Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro Glu Met Thr Thr
 35 40 45
 Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg Thr Thr Pro Glu
 50 55 60
 Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr Ala Thr Thr Thr
 65 70 75 80
 Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr Thr Gln Val Thr
 85 90 95
 Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile Thr Thr Leu Lys
 100 105 110
 Thr Thr Leu Ala Pro Lys Val Thr Thr Lys Lys Thr Ile Thr Thr
 115 120 125
 Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys Pro Lys Asp Arg
 130 135 140
 Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln Lys Pro Thr Lys
 145 150 155 160
 Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys Thr Met Pro Arg
 165 170 175
 Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys Met Thr Ser Thr
 180 185 190

Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu Ala Met Leu Gln
 195 200 205
 Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys Leu Val Glu Val
 210 215 220
 Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly Glu Thr Pro His
 225 230 235 240
 Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val Thr Pro Asp Met
 245 250 255
 Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile Ile Asn Pro Met
 260 265 270
 Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro Val Asp Gly Leu
 275 280 285
 Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg Gly His Tyr Phe
 290 295 300
 Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala Arg Arg Ile Thr
 305 310 315 320
 Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val Phe Thr Arg Cys
 325 330 335
 Asn Cys Glu Gly Lys Thr Phe Phe Lys Asp Ser Gln Tyr Trp Arg
 340 345 350
 Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro Lys Pro Ile Phe Lys
 355 360 365
 Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala Ala Leu Ser Thr Ala
 370 375 380
 Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe Phe Lys Arg Gly Gly
 385 390 395 400
 Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro Val Gln Lys Cys Pro
 405 410 415
 Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr Gly Glu Met Thr Gln
 420 425 430
 Val Arg Arg Arg Phe Glu Arg Ala Ile Gly Pro Ser Gln Thr His
 435 440 445
 Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu Ala Tyr Gln Asp Lys
 450 455 460
 Gly Val Leu His Asn Glu Val Lys Val Ser Ile Leu Trp Arg Gly Leu
 465 470 475 480
 Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro Asn Ile Arg Lys Pro
 485 490 495
 Asp Gly Tyr Asp Tyr Tyr Ala Phe Ser Lys Asp Gln Tyr Tyr Asn Ile
 500 505 510
 Asp Val Pro Ser Arg Thr Ala Arg Ala Ile Thr Thr Arg Ser Gly Gln
 515 520 525
 Thr Leu Ser Lys Val Trp Tyr Asn Cys Pro
 530 535

<210> 4

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<221> VARIANT
<222> 2
<223> Xaa is any amino acid except Pro

<221> VARIANT
<222> 3
<223> Xaa is either Thr or Ser

<400> 4
Asn Xaa Xaa
1

<210> 5
<211> 488
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 5
atgcatgaaa cattccatta ctgtgttctg tgttgttct gatcacaatt tatccaaatt 60
atcagcgtga ggagagtggg agggatttag gatccactga acgtgttaaa cgtcacatac 120
tgggtgtgcc tggtaaggaa gctgactcg gcttccgtaa ggcgcgcttg atcctcgag 180
gggggggggtgg acgcgcgcca agtagaatat acagtgtgtc cgtagaggt ttctgtgcag 240
aagtaaaaaga taacaagaag aacagaacta aaaagaaacc tacccccaaa ccaccagttg 300
tagatgaagc tggaaagtggg ttggacaatg gtgacttcaa ggtcacaact cctgacacgt 360
ctaccaccca acacaataaa gtcagcacat ctcccaagat cacaacagca aaaccaataa 420
atcccagacc ccagtcctca cctaattctg atacatctaa agagacgtct ttgacagtga 480
ataaagag 488

<210> 6
<211> 1620
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 6
cctaccacta tcccacaaaaag coctgatgaa tcaactcctg agctttctgc agaacccaca 60
ccaaaagctc ttgaaaacag tcccaaggaa cctggtgtac ctacaactaa gactcctgca 120
gogactaaac ctgaaatgac tacaacagct aaagacaaga caacagaaag agacttacgt 180
actacacctg aaactacaac tgctgcacct aagatgacaa aagagacagc aactacaaca 240
gaaaaaaaaacta ccgaatccaa aataacagct acaaccacac aagtaacatc taccacaact 300
caagatacca caccatccaa aattactact cttaaaaccaa ctactcttgc acccaaagta 360
actacaacaa aaaagacaat tactaccact gagattatga acaaacctga agaaacagct 420
aaacccaaaag acagagctac taattctaaa gcgacaactc ctaaacctca aaagccaaacc 480

aaagcaccca	aaaaacccac	ttctaccaaa	aagccaaaaa	caatgcctag	agtgagaaaa	540
ccaaagacga	caccaactcc	ccgcaagatg	acatcaacaa	tgccagaatt	gaaccctacc	600
tcaagaatag	cagaagccat	gctccaaacc	accaccagac	ctaaccaaac	tccaaactcc	660
aaactagttg	aagtaaatcc	aaagagtcaa	gatgcaggtg	gtgctgaagg	agaaacacct	720
catatgcttc	tcaggccccca	tgtgttcatg	cctgaagtta	ctcccgacat	ggattactta	780
ccgagagtagc	ccaatcaagg	cattatcatc	aatcccattgc	tttccgatga	gaccaatata	840
tgcaatggta	agccagtaga	tggactgact	actttgcgc	atgggacatt	agttgcattc	900
cgaggtcatt	atttctggat	gctaagtcca	ttcagtccac	catctccagc	tcgcagaatt	960
actgaagttt	ggggatttcc	ttccccatt	gatactgttt	ttactagtg	caactgtgaa	1020
ggaaaaaactt	tcttcattaa	ggattctcag	tactggcgtt	ttaccaatga	tataaaagat	1080
gcagggttacc	ccaaaccaat	tttcaaaggaa	tttggaggac	taactggaca	aatagtggca	1140
gchgcttcaa	cagctaaata	taagaactgg	cctgaatctg	tgtatttttt	caagagaggt	1200
ggcagcattc	agcagtatat	ttataaacag	gaacctgtac	agaagtgc	tggaagaagg	1260
cctgctctaa	attatccagt	gtatggagaa	atgacacagg	ttaggagacg	tcgccttgaa	1320
cgtgctatag	gacccctc	aacacacacc	atcagaattc	aatattcacc	tgccagactg	1380
gcttatcaag	acaaagggtgt	ccttcataat	gaagttaaag	tgagtatact	gtggagagga	1440
cttccaaatg	tggttacctc	agctataatca	ctgccaaca	tcagaaaacc	tgacggctat	1500
gattactatg	cctttctaa	agatcaatac	tataacattg	atgtgcctag	tagaacagca	1560
agagcaatta	ctactcggtc	tgccagacc	ttatccaaag	tctggtacaa	ctgtccttag	1620

<210> 7

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 7

atggcatgga aaacacttcc catt

24

<210> 8

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 8

ctaaggacag ttgtaccaga cttt

24

<210> 9

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 9
Phe Ala Cys Glu
1

<210> 10
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 10
Val Lys Asp Asn Lys Lys Asn Arg
1 5

<210> 11
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<221> VARIANT
<222> 8
<223> Xaa is either Thr or Pro

<400> 11
Lys Glu Pro Ala Pro Thr Thr Xaa
1 5
2
5

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